

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 09 | 856,812B
Source: IFW16
Date Processed by STIC: 11/07/2005

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IFW

IFW16

RAW SEQUENCE LISTING

DATE: 11/07/2005

PATENT APPLICATION: US/09/856,812B

TIME: 12:22:40

Input Set : A:\L0461.70115US00 SEQUENCE LISTING (SECOND REVISION).txt

Output Set: N:\CRF4\11072005\I856812B.raw

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3 <110> APPLICANT: Huang, Lan-Qing
4     Van Pel, Aline
5     Brasseur, Francis
6     De Plaen, Etienne
7     Boon, Thierry
9 <120> TITLE OF INVENTION: Tumour Rejection Antigens
11 <130> FILE REFERENCE: L0461.70115US00
13 <140> CURRENT APPLICATION NUMBER: US 09/856,812B
-> 14 <141> CURRENT FILING DATE: 2001-09-07
16 <150> PRIOR APPLICATION NUMBER: GB 9826143.1
17 <151> PRIOR FILING DATE: 1998-11-27
19 <160> NUMBER OF SEQ ID NOS: 57
21 <170> SOFTWARE: PatentIn Ver. 3.2
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24 <211> LENGTH: 369
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
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33          20          25          30
35 Ala  Val  Glu  Glu  Asp  Ala  Ser  Ser  Ser  Thr  Ser  Thr  Ser  Ser  Ser  Phe
36          35          40          45
38 Pro  Ser  Ser  Phe  Pro  Ser  Ser  Ser  Ser  Ser  Ser  Ser  Ser  Ser  Cys  Tyr
39          50          55          60
41 Pro  Leu  Ile  Pro  Ser  Thr  Pro  Glu  Glu  Val  Ser  Ala  Asp  Asp  Glu  Thr
42  65          70          75          80
44 Pro  Asn  Pro  Pro  Gln  Ser  Ala  Gln  Ile  Ala  Cys  Ser  Ser  Pro  Ser  Val
45          85          90          95
47 Val  Ala  Ser  Leu  Pro  Leu  Asp  Gln  Ser  Asp  Glu  Gly  Ser  Ser  Ser  Gln
48          100         105         110
50 Lys  Glu  Glu  Ser  Pro  Ser  Thr  Leu  Gln  Val  Leu  Pro  Asp  Ser  Glu  Ser
51          115         120         125
53 Leu  Pro  Arg  Ser  Glu  Ile  Asp  Glu  Lys  Val  Thr  Asp  Leu  Val  Gln  Phe
54          130         135         140
56 Leu  Leu  Phe  Lys  Tyr  Gln  Met  Lys  Glu  Pro  Ile  Thr  Lys  Ala  Glu  Ile
57 145          150         155         160
59 Leu  Glu  Ser  Val  Ile  Lys  Asn  Tyr  Glu  Asp  His  Phe  Pro  Leu  Leu  Phe
60          165         170         175
62 Ser  Glu  Ala  Ser  Glu  Cys  Met  Leu  Leu  Val  Phe  Gly  Ile  Asp  Val  Lys
63          180         185         190
65 Glu  Val  Asp  Pro  Thr  Gly  His  Ser  Phe  Val  Leu  Val  Thr  Ser  Leu  Gly

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72 225      230      235      240
74 Thr Pro Glu Glu Val Ile Trp Glu Ala Leu Asn Met Met Gly Leu Tyr
75      245      250      255
77 Asp Gly Met Glu His Leu Ile Tyr Gly Glu Pro Arg Lys Leu Leu Thr
78      260      265      270
80 Gln Asp Trp Val Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly
81      275      280      285
83 Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala His Ala
84      290      295      300
86 Glu Ile Arg Lys Met Ser Leu Leu Lys Phe Leu Ala Lys Val Asn Gly
87 305      310      315      320
89 Ser Asp Pro Arg Ser Phe Pro Leu Trp Tyr Glu Glu Ala Leu Lys Asp
90      325      330      335
92 Glu Glu Glu Arg Ala Gln Asp Arg Ile Ala Thr Thr Asp Asp Thr Thr
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115      35      40      45
117 Thr Leu Glu Glu Val Thr Asp Ser Gly Ser Pro Ser Pro Pro Gln Ser
118      50      55      60
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121 65      70      75      80
123 Ser Gln Ser Asp Glu Gly Ser Ser Ser Asn Glu Glu Glu Gly Pro Ser
124      85      90      95
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133      130      135      140
135 Asn Tyr Lys Asn His Phe Pro Asp Ile Phe Ser Lys Ala Ser Glu Cys
136 145      150      155      160
138 Met Gln Val Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Gly
139      165      170      175

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141 His Ser Tyr Ile Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu
142          180          185          190
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147 Leu Gly Met Ile Leu Met Glu Gly Ser Arg Ala Pro Glu Glu Ala Ile
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150 Trp Glu Ala Leu Ser Val Met Gly Ala Val
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166 tgtccccctc ccttgcccac ccccccccc ccccccgcca aatgtctgct ctttctgtca 180
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177 ccctactgtc actctggaga acccagtcag ggctgtccgc tgagtctccc tgtcttatac 840
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197 cacactccca cctgctaccc tgatcagagt catc atg cct cga gct cca aag cgt 1975

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203			10				15	
205	ggc	ctc	gag	ggg	gca	cag	gct	ccc
206	Gly	Leu	Glu	Gly	Ala	Gln	Ala	Pro
207		25					30	
209	tca	tcc	act	tcc	acc	agc	tcc	tct
210	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ser
211	40						45	
213	tcc	tct	tcc	tcc	tcc	tcc	tcc	tgc
214	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Cys
215					60			65
217	gag	gag	gtt	tct	gct	gat	gat	gag
218	Glu	Glu	Val	Ser	Ala	Asp	Asp	Glu
219			75					80
221	cag	ata	gcc	tgc	tcc	tcc	ccc	tcg
222	Gln	Ile	Ala	Cys	Ser	Ser	Pro	Ser
223			90					95
225	caa	tct	gat	gag	ggc	tcc	agc	agc
226	Gln	Ser	Asp	Glu	Gly	Ser	Ser	Ser
227		105						110
229	cta	cag	gtc	ctg	cca	gac	agt	gag
230	Leu	Gln	Val	Leu	Pro	Asp	Ser	Glu
231	120							125
233	gaa	aag	gtg	act	gat	ttg	gtg	cag
234	Glu	Lys	Val	Thr	Asp	Leu	Val	Gln
235					140			145
237	aag	gag	ccg	atc	aca	aag	gca	gaa
238	Lys	Glu	Pro	Ile	Thr	Lys	Ala	Glu
239			155					160
241	tat	gaa	gac	cac	ttc	cct	ttg	ttg
242	Tyr	Glu	Asp	His	Phe	Pro	Leu	Leu
243			170					175
245	ctg	ctg	gtc	ttt	ggc	att	gat	gta
246	Leu	Leu	Val	Phe	Gly	Ile	Asp	Val
247		185						190
249	tcc	ttt	gtc	ctt	gtc	acc	tcc	ctg
250	Ser	Phe	Val	Leu	Val	Thr	Ser	Leu
251	200							205
253	agt	gat	gtc	cag	agc	atg	ccc	aag
254	Ser	Asp	Val	Gln	Ser	Met	Pro	Lys
255					220			225
257	agc	ata	atc	ttc	ata	gag	ggc	tac
258	Ser	Ile	Ile	Phe	Ile	Glu	Gly	Tyr
259			235					240
261	gaa	gca	ctg	aat	atg	atg	ggg	ctg
262	Glu	Ala	Leu	Asn	Met	Met	Gly	Leu

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267          265          270          275
269 tac ctg gag tac cgg cag gtg cct ggc agt gat cct gca cgg tat gag 2839
270 Tyr Leu Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Arg Tyr Glu
271 280          285          290          295
273 ttt ctg tgg ggt cca agg gct cat gct gaa att agg aag atg agt ctc 2887
274 Phe Leu Trp Gly Pro Arg Ala His Ala Glu Ile Arg Lys Met Ser Leu
275          300          305          310
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279          315          320          325
281 ctg tgg tat gag gag gct ttg aaa gat gag gaa gag aga gcc cag gac 2983
282 Leu Trp Tyr Glu Glu Ala Leu Lys Asp Glu Glu Glu Arg Ala Gln Asp
283          330          335          340
285 aga att gcc acc aca gat gat act act gcc atg gcc agt gca agt tct 3031
286 Arg Ile Ala Thr Thr Asp Asp Thr Thr Ala Met Ala Ser Ala Ser Ser
287          345          350          355
289 agc gct aca ggt agc ttc tcc tac cct gaa taa agtaagacag attcttcact 3084
290 Ser Ala Thr Gly Ser Phe Ser Tyr Pro Glu
-> 291 360          365          370
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291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5